

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 8, 2003, 14:57:25 ; Search time 96 Seconds  
(without alignments)  
1446.622 Million cell updates/sec

Title: US-09-462-517-1

Perfect score: 3490  
Sequence: 1 MVQFLGKGTAGELIHWTL.....KSMETVTRPKPLTEAPKA 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_21:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_protist:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriophage:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3317	95.0	674	5	Q24008
2	3312	94.9	674	5	Q9NBV3
3	2136	61.2	665	5	Q23823
4	544.5	15.6	2042	4	Q75970
5	523	15.0	2055	11	Q8VBX6
6	523	15.0	2055	11	Q8VBX6
7	519	14.9	2055	11	Q921K3
8	519	14.9	2055	11	Q8VBX0
9	508	14.6	2054	11	Q55164
10	490	14.0	1134	4	Q9H3N9
11	427.5	12.2	2208	5	Q09515
12	419	12.0	1552	4	Q60833
13	411	11.8	1582	4	Q43742
14	384	11.0	1524	4	Q15249
15	345.5	9.9	612	11	Q70471
16	253	7.2	1695	5	Q9BKL2

17	246.5	7.1	582	4	Q8WX31	Q8WX31 homo sapien
18	239	6.8	51	5	Q9TW8	Q9TW8 calliphora
19	239	6.8	526	11	Q08783	Q08783 mus musculus
20	235	6.7	453	4	Q43798	Q43798 homo sapien
21	231.5	6.6	2460	11	Q64512	Q64512 mus musculus
22	229	6.6	2484	6	Q28006	Q28006 bos taurus
23	221.5	6.3	1163	13	Q9YHW2	Q9YHW2 gallus gall
24	210	6.0	1663	11	Q8V111	Q8V111 mus musculus
25	203	5.8	346	11	Q9CS43	Q9CS43 mus musculus
26	201.5	5.8	871	5	Q9XZ35	Q9XZ35 drosophila
27	200.5	5.7	2766	11	Q9QZ88	Q9QZ88 rattus norv
28	199.5	5.7	871	5	Q9NB04	Q9NB04 drosophila
29	198.5	5.7	904	11	Q921G9	Q921G9 mus musculus
30	198.5	5.7	721	11	Q91WJ1	Q91WJ1 mus musculus
31	198.5	5.7	1256	4	Q75085	Q75085 homo sapien
32	198	5.7	346	4	Q8WU78	Q8WU78 homo sapien
33	196	5.6	944	11	Q922S3	Q922S3 mus musculus
34	193.5	5.5	1287	4	Q96029	Q96029 homo sapien
35	193	5.5	1462	4	Q96027	Q96027 homo sapien
36	191	5.5	1564	4	Q14160	Q14160 homo sapien
37	191	5.5	1630	4	Q8WV8	Q8WV8 homo sapien
38	190.5	5.5	1179	11	Q9JK71	Q9JK71 rattus norv
39	189.5	5.4	1114	11	Q9R271	Q9R271 rattus norv
40	189.5	5.4	1126	11	Q9EQ39	Q9EQ39 mus musculus
41	189.5	5.4	1277	11	Q8B382	Q8B382 rattus norv
42	184.5	5.3	632	4	Q8BY20	Q8BY20 homo sapien
43	184.5	5.3	728	4	Q8TB81	Q8TB81 homo sapien
44	182.5	5.2	687	11	Q91XL2	Q91XL2 mus musculus
45	182.5	5.2	960	5	Q9VY25	Q9VY25 drosophila

## ALIGNMENTS

RESULT 1	ID	Q24008	PRELIMINARY:	PRT:	674 AA.
AC	Q24008	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)				
DR	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	INAD protein.				
OS	INAD OR CG3504.				
GN	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	STRAIN-BERKELEY;				
RX	MEDLINE-20196006; PubMed-10731132;				
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,				
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,				
RA	Borova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,				
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durkin K.J., Evangelista C.C., Ferraz C., Ferrelia S., Fleischmann W.,				
RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,				
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,				
RA	Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Mosher A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.H., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusslein-Volhard C., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos K., Simpson M., Skupski M.P., Smith T.,  
 RA Spletter E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtsek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RT Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RT Science 287:2185-2195 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE;  
 RA Lindsley D.L., Zimm G.G.;  
 RT "The genome of *Drosophila melanogaster*.";  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE;  
 RX MEDLINE-95127229; PubMed-782638;  
 RA Shieh B.H., Niemeyer B.;  
 RT "A novel protein encoded by the *Inad* gene regulates recovery of visual  
 RT transduction in *Drosophila*.";  
 RL Neuron 14:201-210 (1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE;  
 RA Shieh B.;  
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE;  
 RA Shieh B.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE003458; AAF6915.1;  
 DR EMBL: U15803; AAC36490.1;  
 DR HSSP: P31016; 1BFE.  
 DR FlyBase: FBgn0001263; *Inad*.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ: 5.  
 DR SMART: SM00228; PDZ: 5.  
 DR PROSITE: PS50106; PDZ: 5.  
 SQ SEQUENCE 674 AA; 74332 MW; DAC24091D99EA7F3 CRC64;  
 Query Match 95.0%; Score 3317; DB 5; Length 674;  
 Best Local Similarity 95.3%; Pred. No. 2.5e-200;  
 Matches 654; Conservative 1; Mismatches 7; Indels 24; Gaps 3;  
 QY 1 MVQFLGKGTAGELIHMVTLDTKTKSGFICIVRGVDSPTTKTGFIFGIYVDSPAH 60  
 DB 1 MVQFLGKGTAGELIHMVTLDTKTKSGFICIVRGVDSPTTKTGFIFGIYVDSPAH 60  
 QY 1 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTFDKSDDEQAKSDPSRN 120  
 DB 1 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTFDKSDDEQAKSDPSRN 120  
 QY 121 GYMAKKNFNEQTTNNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180  
 DB 121 GYMAKKNFNEQTTNNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180  
 QY 181 NYADEDEDDTDMTGRITTEAGYEIDRASAGCNCLINKOEKDRKDEDEDEFGYTA 240  
 DB 181 NYADEDEDDTDMTGRITTEAGYEIDRASAGCNCLINKOEKDRKDEDEDEFGYTA 240  
 QY 241 YNMAKDLRIEVRDASRPLGLALAGHKDRKMACFVAGVDPNGLSGVDIKPGDEIVEY 300  
 DB 241 YNMAKDLRIEVRDASRPLGLALAGHKDRKMACFVAGVDPNGLSGVDIKPGDEIVEY 300

DB 241 YNMAKDLRIEVRDASRPLGLALAGHKDRKMACFVAGVDPNGLSGVDIKPGDEIVEY 300  
 QY 301 NGVVLKRNCHLNASAVFKNVDGKLVITSRKPNDEGMCKPKIKFPASDETKFI 360  
 DB 301 NGVVLKRNCHLNASAVFKNVDGKLVITSRKPNDEGMCKPKIKFPASDETKFI 360  
 QY 361 FPKARFVQVKEEFLIMVYTGKHAEGSGIFISDLREGSNALACVKGVDMLANOV 420  
 DB 361 FPKARFVQVKEEFLIMVYTGKHAEGSGIFISDLREGSNALACVKGVDMLANOV 420  
 QY 421 TLESNDATGTLKRAEGVVTMLTLKSEAIKAERKEEKEEKEEKEEKEEKEE 480  
 DB 421 TLESNDATGTLKRAEGVVTMLTLKSEAIKAERKEEKEEKEEKEEKEEKEE 480  
 QY 481 EIRPNKKILIELKVEKPKCHLRKOKOPCHMILC-----NPRLS-----GGQVAA 528  
 DB 481 EIRPNKKILIELKVEKPKCHLRKOKOPCHMILC-----NPRLS-----GGQVAA 528  
 QY 529 DKRLKIFDHIDINGTPIHVGSMVTLKHQLPHTTEKAVTLVFRADPELEKFNVD 588  
 DB 529 DKRLKIFDHIDINGTPIHVGSMVTLKHQLPHTTEKAVTLVFRADPELEKFNVD 588  
 QY 589 KRAGKELGSLSPNEIGCTIADLIQGYPEIDSKLORGDIITFKNGDALEGLFPQV 648  
 DB 589 KRAGKELGSLSPNEIGCTIADLIQGYPEIDSKLORGDIITFKNGDALEGLFPQV 648  
 QY 649 FKGANKEVMEYTRPPTLTETPAKA 674  
 DB 649 FKGANKEVMEYTRPPTLTETPAKA 674  
 RESULT 2  
 Q9NBV3 PRELIMINARY; PRT; 674 AA.  
 AC Q9NBV3;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE INAD.  
 GN INAD OR CG3504.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CANTON-S;  
 RA Ashari M., Shieh B.;  
 RT "The *Inad* locus in *Drosophila*.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF245280; AAF81203.1;  
 DR HSSP: P31016; 1BFE.  
 DR FlyBase: FBgn0001263; *Inad*.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ: 5.  
 DR SMART: SM00228; PDZ: 5.  
 DR PROSITE: PS50106; PDZ: 5.  
 SQ SEQUENCE 674 AA; 74305 MW; 55B1C57B7A100FID CRC64;  
 Query Match 94.9%; Score 3312; DB 5; Length 574;  
 Best Local Similarity 95.2%; Pred. No. 5.1e-200;  
 Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;  
 QY 1 MVQFLGKGTAGELIHMVTLDTKTKSGFICIVRGVDSPTTKTGFIFGIYVDSPAH 60  
 DB 1 MVQFLGKGTAGELIHMVTLDTKTKSGFICIVRGVDSPTTKTGFIFGIYVDSPAH 60  
 QY 61 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTFDKSDDEQAKSDPSRN 120  
 DB 61 CGRLKVGDRILSLNGKVRNSTEAVIDLKKEADFKLEIQTFDKSDDEQAKSDPSRN 120  
 QY 121 GYMAKKNFNEQTTNNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180  
 DB 121 GYMAKKNFNEQTTNNNASGGGOGGOGGOGGAGNRRQOSMOKRNTTFTASRKH 180

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 8, 2003, 14:57:17 ; Search time 40 Seconds

(Without alignments)  
2245.273 Million cell updates/sec

Title: US-09-462-517-1

Perfect score: 3490

Sequence: 1 WQFLGKQGTAGELIHVTL.....KVSMEVTRPKPLTEAPKA 674

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq.101002.\*

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- 4: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT.\*
- 5: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT.\*
- 6: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT.\*
- 7: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT.\*
- 8: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT.\*
- 9: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT.\*
- 10: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT.\*
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- 20: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT.\*
- 21: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT.\*
- 22: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.\*
- 23: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3490	100.0	674	20	AAW92953
2	3317	95.0	674	22	ABBS9957
3	539	15.4	1111	23	AAU87918
4	537	15.4	2037	21	AAV53753
5	533.5	15.3	2070	20	AAV04733
6	523.5	15.0	856	21	AAU01383
7	508	14.6	1373	20	AAV04730
8	508	14.6	2000	20	AAV04732
9	505.5	14.5	1005	20	AAV04731
10	491	14.1	1881	20	AAV24025

11	460	13.2	1627	22	ABG06117	Novel: human diapo
12	446.5	12.8	763	20	AAV04741	PDZ domain-contain
13	419	12.0	1552	22	AAW87893	Human protein SEQ
14	419	12.0	1554	22	ABG07288	Novel: human diapo
15	411	11.8	1584	22	ABG07290	Novel: human diapo
16	384	11.0	1526	22	ABG06116	Novel: human diapo
17	384	11.0	1526	22	ABG07289	Novel: human diapo
18	384	11.0	1526	22	AAW79777	Human protein SEQ
19	241.5	6.9	2485	21	AAV19343	Amlyc acid sequenc
20	238.5	6.8	2466	16	AAW71498	Human protein tyro
21	238.5	6.8	2466	21	AAV5999	Intracellular proto
22	238.5	6.8	2466	21	AAV90272	Human PTPBL phosph
23	228	6.3	206	20	AAV74151	Human prostate tum
24	220	6.3	318	20	AAV74150	Human prostate tum
25	209.5	6.0	1239	20	AAV04734	Protein containing
26	206.5	5.9	354	23	AAU87920	Human PDZ3 protei
27	201.5	5.8	871	22	ABBS7855	Drosophila melanog
28	201.5	5.8	871	22	ABBS7855	Drosophila melanog
29	200.5	5.7	928	23	AAE21718	Human PKIN-13 prot
30	200.5	5.7	1037	22	ABG22366	Novel: human diagr
31	199	5.7	724	23	ABB04799	LDL receptor bindi
32	196.5	5.6	724	23	ABB04798	LDL receptor bindi
33	196.5	5.6	767	21	AAU82138	Human post-synapti
34	196.5	5.6	767	23	AAU84269	Human endometrial
35	196.5	5.6	767	23	AAU84328	Protein DLG4 diffe
36	191	5.5	1535	23	AAU87934	Human protein cont
37	189.5	5.4	1277	21	AAU80149	Rat synaptic scaff
38	188.5	5.4	632	21	AAU801385	Human polyepitide
39	186.5	5.3	304	22	AAW93296	Human post-synapti
40	185	5.3	344	22	ABBS5834	PDZ encoded domain
41	185	5.3	344	22	ABBS7623	Human post-synapti
42	185	5.3	344	22	ABBS5035	Human post-synapti
43	184.5	5.3	469	22	AAU40870	Human polyepitide
44	184.5	5.3	590	20	AAV04736	PDZ domain-contain
45	184.5	5.3	632	21	AAV66689	Membrane-bound pro

#### ALIGNMENTS

RESULT 1	AAW92953	standard: Protein; 674 AA.
XX	AAW92953:	
AC	14-MAY-1999 (first entry)	
XX		
DT	Fly transducinome Inad protein.	
XX		
DE	Inad: transducinome; fly; insect; signal transduction protein; mutant;	
XX	PDZ domain; modulator; cell surface receptor; ion channel; treatment;	
KW	disorder.	
XX		
OS	Insecta.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 319	/note= "encoded by AGC"
FT	Misc-difference 501	/note= "Encoded by GT"
FT	Misc-difference 508	/note= "Encoded by GAA"
FT	Misc-difference 524	/note= "Encoded by GGA"
FT		
XX	W09903974-A1.	
XX		
PN	28-JAN-1999.	
XX		
PD	15-JUL-1998;	98MO-US14667.
XX		
PF	15-JUL-1997;	97US-0052588.
XX		
PR		



RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattle B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazuelo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,  
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spleer E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE.  
 RA Lindsley D.L., Zimm G.G.;  
 RT "The genome of *Drosophila melanogaster*.";  
 RL submitted (Feb-1995) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE.  
 RX MEDLINE-95127229; PubMed-7826638;  
 RA Shieh B.H., Niemeyer B.;  
 RT "A novel protein encoded by the *Inad* gene regulates recovery of visual  
 RL transduction in *Drosophila*.";  
 RL Neuron 14:201-210(1995).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE.  
 RA Shieh B.;  
 RL Submitted (Oct-1994) to the EMBL/GenBank/DBJ databases.  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-COMPOUND EYE.  
 RA Shieh B.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE003458; AAF46915.1;  
 DR EMBL: U15803; AAC36490.1;  
 DR HSSP: P31016; 1BFE.  
 DR Flybase: FBgn0001263; *Inad*.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ; 5.  
 DR SMART: SM00228; PDZ; 5.  
 DR PROSITE: PS50106; PDZ; 5.  
 SQ SEQUENCE 674 AA; 74332 MW; D4C24091D99EATF3 CRC64;  
 Query Match 95.0%; Score 3317; DB 5; Length 674;  
 Best Local Similarity 95.3%; Pred. No. 2.5e-200;  
 Matches 654; Conservative 1; Mismatches 7; Indels 24; Gaps 3;  
 QY 1 MVQFLKQGTAGELIHVTLDTKTKSFGICIRGEVKDPSNRTTGIPIKIGVPSPAH 60  
 DB 1 MVQFLKQGTAGELIHVTLDTKTKSFGICIRGEVKDPSNRTTGIPIKIGVPSPAH 60  
 QY 61 LCGRLKVGRIILSLNKGVDVNSTEQAVIDLKFADEKIELEIOTFSDSQOAKSDPSRN 120  
 DB 61 LCGRLKVGRIILSLNKGVDVNSTEQAVIDLKFADEKIELEIOTFSDSQOAKSDPSRN 120  
 QY 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTASMKQKHS 180  
 DB 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTASMKQKHS 180  
 QY 181 NVADEDEDEPTDRTGRIIRFAGYEIRASAGNCKLKOEKDRDKEDEFGYTMATINKR 240  
 DB 181 NVADEDEDEPTDRTGRIIRFAGYEIRASAGNCKLKOEKDRDKEDEFGYTMATINKR 240  
 QY 241 YNNMKDLRIEVOBRSKPLGLAGHKDROKACPVAGVDPNGALGSVDIKGDEIVEY 300  
 DB 241 YNNMKDLRIEVOBRSKPLGLAGHKDROKACPVAGVDPNGALGSVDIKGDEIVEY 300  
 DB 241 YNNMKDLRIEVOBRSKPLGLAGHKDROKACPVAGVDPNGALGSVDIKGDEIVEY 300  
 QY 301 NNNVTLKRNCHLASAVFKNVDDKLVITSRKRPNDGNCVPIKKEPTASDETKRIFDQ 360  
 DB 301 NNNVTLKRNCHLASAVFKNVDDKLVITSRKRPNDGNCVPIKKEPTASDETKRIFDQ 360  
 QY 361 NNNVTLKRNCHLASAVFKNVDDKLVITSRKRPNDGNCVPIKKEPTASDETKRIFDQ 360  
 DB 361 NNNVTLKRNCHLASAVFKNVDDKLVITSRKRPNDGNCVPIKKEPTASDETKRIFDQ 360  
 QY 361 PFKATVOYRKKEGFGIMVITGKHAEVGSGITISDLRESNMLAGVYGMULLAVNDV 420  
 DB 361 PFKATVOYRKKEGFGIMVITGKHAEVGSGITISDLRESNMLAGVYGMULLAVNDV 420  
 QY 421 TLESYVDATGILKRAEGVWILLTLKSEENIKAEKAEKKEEKEEKEEKEEKEEKEE 480  
 DB 421 TLESYVDATGILKRAEGVWILLTLKSEENIKAEKAEKKEEKEEKEEKEEKEEKEE 480  
 QY 481 EKKPKKTLIELKVKKKRMGCHRLAROKPCDMLC-----NHPRLS-----GGVAA 528  
 DB 481 EKKPKKTLIELKVKKKRMGCHRLAROKPCDMLC-----NHPRLS-----GGVAA 528  
 QY 529 DKRLKIFDHIDINCTPIVGSMTLKVHOLEFHTTEKRAVTLTPRADPELEKPNVLM 588  
 DB 529 DKRLKIFDHIDINCTPIVGSMTLKVHOLEFHTTEKRAVTLTPRADPELEKPNVLM 588  
 QY 589 KKAGKEGLSLSPNEIGCTIADLIQGYPEIDSKLQRGDIITKFGDLEGLPEOVCYAL 648  
 DB 589 KKAGKEGLSLSPNEIGCTIADLIQGYPEIDSKLQRGDIITKFGDLEGLPEOVCYAL 648  
 QY 649 FKANGKVMETRPKPLTRTEAPRA 674  
 DB 649 FKANGKVMETRPKPLTRTEAPRA 674  
 RESULT 2  
 Q9NBV3 PRELIMINARY; PRT: 674 AA.  
 AC Q9NBV3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE *INAD*.  
 GN *INAD* OR CG3504.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 NX NCBL\_TaxID=7227;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CANTON-S;  
 RA Ashari M., Shieh B.;  
 RT "The *Inad* locus in *Drosophila*.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AAF45280; AAF81203.1;  
 DR HSSP: P31016; 1BFE.  
 DR Flybase: FBgn0001263; *Inad*.  
 DR InterPro: IPR001478; PDZ.  
 DR Pfam: PF00595; PDZ; 5.  
 DR SMART: SM00228; PDZ; 5.  
 DR PROSITE: PS50106; PDZ; 5.  
 SQ SEQUENCE 674 AA; 74305 MW; 55B1C57B7A10F1D CRC64;  
 Query Match 94.9%; Score 3312; DB 5; Length 674;  
 Best Local Similarity 95.2%; Pred. No. 5.1e-200;  
 Matches 653; Conservative 2; Mismatches 7; Indels 24; Gaps 3;  
 QY 1 MVQFLKQGTAGELIHVTLDTKTKSFGICIRGEVKDPSNRTTGIPIKIGVPSPAH 60  
 DB 1 MVQFLKQGTAGELIHVTLDTKTKSFGICIRGEVKDPSNRTTGIPIKIGVPSPAH 60  
 QY 61 LCGRLKVGRIILSLNKGVDVNSTEQAVIDLKFADEKIELEIOTFSDSQOAKSDPSRN 120  
 DB 61 LCGRLKVGRIILSLNKGVDVNSTEQAVIDLKFADEKIELEIOTFSDSQOAKSDPSRN 120  
 QY 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTASMKQKHS 180  
 DB 121 GYVQAKNKNFNOGTNNNNSGGGGMGGGGMGGGMNROSGMOKRNTFTASMKQKHS 180